



E)

		Smp_000700	Human template (5EX3)
RAMPAGE	Number of residues in favoured region (~98.0% expected)	88.60%	97.90%
	Number of residues in allowed region (~2.0% expected)	10%	2.10%
	Number of residues in outlier region	1.50%	0
ProSA-web	Z-score	-7.48	-9.8
ERRAT	Good high resolution structures around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%	88.15%	95.93%
Verify 3D	80% of the amino acids have scored >= 0.2	81.90%	99.07%